



1

SEQUENCE LISTING

MAY 18 2000
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Whitney, Michael
Cubitt, Andrew B.
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<120> METHODS OF PROTEIN DESTABILIZATION AND
USES THEREOF

<130> AURO1330

<140> 09/498,098

<141> 2000-02-04

<160> 74

<170> FastSEQ for Windows Version 4.0

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<211> 6

<212> PRT

<213> Eukaryote

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cagaggttga	tctttgctgg	gaaacagctg	gaagatggac	gcaccctgtc	tgactacaac	180
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<211> 795

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<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(795)

<223> cloning vector

<400> 3

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atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg agc act Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr 35 40 45	144
ttt aaa gtt ctg cta tgt ggc gcg gta tta tcc cgt gtt gac gcc ggg Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Val Asp Ala Gly 50 55 60	192
caa gag caa ctc ggt cgc cgc ata cac tat tct cag aat gac ttg gtt Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser Gln Asn Asp Leu Val 65 70 75 80	240
gag tac tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val 85 90 95	288
aga gaa tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala 100 105 110	336
aac tta ctt ctg aca acg atc gga gga ccg aag gag cta acc gct ttt Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe 115 120 125	384
ttg cac aac atg ggg gat cat gta act cgc ctt gat cgt tgg gaa ccg Leu His Asn Met Gly Asp His Val Thr Arg Leu Asp Arg Trp Glu Pro 130 135 140	432
gag ctg aat gaa gcc ata cca aac gac gag cgt gac acc acg atg cct Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro 145 150 155 160	480
gca gca atg gca aca acg ttg cgc aaa cta tta act ggc gaa cta ctt Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu 165 170 175	528
act cta gct tcc cgg caa caa tta ata gac tgg atg gag gcg gat aaa Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys 180 185 190	576
gtt gca gga cca ctt ctg cgc tcg gcc ctt ccg gct ggc tgg ttt att Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile 195 200 205	624
gct gat aaa tct gga gcc ggt gag cgt ggg tct cgc ggt atc att gca Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala 210 215 220	672
gca ctg ggg cca gat ggt aag ccc tcc cgt atc gta gtt atc tac acg Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr 225 230 235 240	720
acg ggg agt cag gca act atg gat gaa cga aat aga cag atc gct gag Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu 245 250 255	768

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 Ile Gly Ala Ser Leu Ile Lys His Trp
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795

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ttt tgc ctt cct gtt ttt ggt cac cca gaa acg ctg gtg aaa gta aaa 96
 Phe Cys Leu Pro Val Phe Gly His Pro Glu Thr Leu Val Lys Val Lys
 20 25 30

gat gct gaa gat cag ttg ggt gca cga gtg ggt tac atc gaa ctg gat 144
 Asp Ala Glu Asp Gln Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp
 35 40 45

ctc aac agc ggt aag atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt 192
 Leu Asn Ser Gly Lys Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe
 50 55 60

cca atg atg agc act ttt aaa gtt ctg cta tgt ggc gcg gta tta tcc 240
 Pro Met Met Ser Thr Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser
 65 70 75 80

cgt gtt gac gcc ggg caa gag caa ctc ggt cgc cgc ata cac tat tct 288
 Arg Val Asp Ala Gly Gln Glu Gln Leu Gly Arg Arg Ile His Tyr Ser
 85 90 95

cag aat gac ttg gtt gag tac tca cca gtc aca gaa aag cat ctt acg 336
 Gln Asn Asp Leu Val Glu Tyr Ser Pro Val Thr Glu Lys His Leu Thr
 100 105 110

gat ggc atg aca gta aga gaa tta tgc agt gct gcc ata acc atg agt 384
 Asp Gly Met Thr Val Arg Glu Leu Cys Ser Ala Ala Ile Thr Met Ser
 115 120 125

gat aac act gcg gcc aac tta ctt ctg aca acg atc gga gga ccg aag 432
 Asp Asn Thr Ala Ala Asn Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys
 130 135 140

gag cta acc gct ttt ttg cac aac atg ggg gat cat gta act cgc ctt 480
 Glu Leu Thr Ala Phe Leu His Asn Met Gly Asp His Val Thr Arg Leu
 145 150 155 160

gat cgt tgg gaa ccg gag ctg aat gaa gcc ata cca aac gac gag cgt 528
 Asp Arg Trp Glu Pro Glu Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg

165	170	175	
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Asp Thr Thr Met Pro Ala Ala Met Ala Thr Thr Leu Arg Lys Leu Leu			
180	185	190	
act ggc gaa cta ctt act cta gct tcc cgg caa caa tta ata gac tgg			624
Thr Gly Glu Leu Leu Thr Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp			
195	200	205	
atg gag gcg gat aaa gtt gca gga cca ctt ctg cgc tcg gcc ctt ccg			672
Met Glu Ala Asp Lys Val Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro			
210	215	220	
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Ala Gly Trp Phe Ile Ala Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser			
225	230	235	240
cgc ggt atc att gca gca ctg ggg cca gat ggt aag ccc tcc cgt atc			768
Arg Gly Ile Ile Ala Ala Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile			
245	250	255	
gta gtt atc tac acg acg ggg agt cag gca act atg gat gaa cga aat			816
Val Val Ile Tyr Thr Thr Gly Ser Gln Ala Thr Met Asp Glu Arg Asn			
260	265	270	
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Leu Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys			
20	25	30	
atc ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg agc act			144
Ile Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr			
35	40	45	
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Phe Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Asp Asp Ala Gly			
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caa gag caa ctc ggt cgc cgc ata cac tat tct cag aat gac ttg gtt			240

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Glu	Tyr	Ser	Pro	Val	Thr	Glu	Lys	His	Leu	Thr	Asp	Gly	Met	Thr	Val	
				85					90					95		
aga gaa tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc																336
Arg	Glu	Leu	Cys	Ser	Ala	Ala	Ile	Thr	Met	Ser	Asp	Asn	Thr	Ala	Ala	
			100					105					110			
aac tta ctt ctg aca acg atc gga gga ccg aag gag cta acc gct ttt																384
Asn	Leu	Leu	Leu	Thr	Thr	Ile	Gly	Gly	Pro	Lys	Glu	Leu	Thr	Ala	Phe	
		115					120					125				
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Leu	His	Asn	Met	Gly	Asp	His	Val	Thr	Arg	Leu	Asp	His	Trp	Glu	Pro	
	130					135					140					
gag ctg aat gaa gcc ata cca aac gac gag cgt gac acc acg atg cct																480
Glu	Leu	Asn	Glu	Ala	Ile	Pro	Asn	Asp	Glu	Arg	Asp	Thr	Thr	Met	Pro	
145					150				155						160	
gta gca atg gca aca acg ttg cgc aaa cta tta act ggc gaa cta ctt																528
Val	Ala	Met	Ala	Thr	Thr	Leu	Arg	Lys	Leu	Leu	Thr	Gly	Glu	Leu	Leu	
				165					170					175		
act cta gct tcc cgg caa caa tta ata gac tgg atg gag gcg gat aaa																576
Thr	Leu	Ala	Ser	Arg	Gln	Gln	Leu	Ile	Asp	Trp	Met	Glu	Ala	Asp	Lys	
			180					185					190			
gtt gca gga cca ctt ctg cgc tcg gcc ctt ccg gct ggc tgg ttt att																624
Val	Ala	Gly	Pro	Leu	Leu	Arg	Ser	Ala	Leu	Pro	Ala	Gly	Trp	Phe	Ile	
		195					200					205				
gct gat aaa tct gga gcc ggt gag cgt ggg tct cgc ggt atc att gca																672
Ala	Asp	Lys	Ser	Gly	Ala	Gly	Glu	Arg	Gly	Ser	Arg	Gly	Ile	Ile	Ala	
	210					215					220					
gca ctg ggg cca gat ggt aag ccc tcc cgt atc gta gtt atc tac acg																720
Ala	Leu	Gly	Pro	Asp	Gly	Lys	Pro	Ser	Arg	Ile	Val	Val	Ile	Tyr	Thr	
225					230					235					240	
acg ggg agt cag gca act atg gat gaa cga aat aga cag atc gct gag																768
Thr	Gly	Ser	Gln	Ala	Thr	Met	Asp	Glu	Arg	Asn	Arg	Gln	Ile	Ala	Glu	
				245				250						255		
ata ggt gcc tca ctg att aag cat tgg																795
Ile	Gly	Ala	Ser	Leu	Ile	Lys	His	Trp								
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<211> 792

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(792)

<223> cloning vector

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ggt gca cga gtg ggt tac atc gaa ctg gat ctc aac agc ggt aag atc	96
Gly Ala Arg Val Gly Tyr Ile Glu Leu Asp Leu Asn Ser Gly Lys Ile	
20 25 30	
ctt gag agt ttt cgc ccc gaa gaa cgt ttt cca atg atg agc act ttt	144
Leu Glu Ser Phe Arg Pro Glu Glu Arg Phe Pro Met Met Ser Thr Phe	
35 40 45	
aaa gtt ctg cta tgt ggc gcg gta tta tcc cgt att gac gcc ggg caa	192
Lys Val Leu Leu Cys Gly Ala Val Leu Ser Arg Ile Asp Ala Gly Gln	
50 55 60	
gag caa ctc ggt cgc cgc ata cac tat tct cag aat gac ttg gtt gag	240
Glu Gln Leu Gly Arg Ile His Tyr Ser Gln Asn Asp Leu Val Glu	
65 70 75 80	
tac tca cca gtc aca gaa aag cat ctt acg gat ggc atg aca gta aga	288
Tyr Ser Pro Val Thr Glu Lys His Leu Thr Asp Gly Met Thr Val Arg	
85 90 95	
gaa tta tgc agt gct gcc ata acc atg agt gat aac act gcg gcc aac	336
Glu Leu Cys Ser Ala Ala Ile Thr Met Ser Asp Asn Thr Ala Ala Asn	
100 105 110	
tta ctt ctg aca acg atc gga gga ccg aag gag cta acc gct ttt ttg	384
Leu Leu Leu Thr Thr Ile Gly Gly Pro Lys Glu Leu Thr Ala Phe Leu	
115 120 125	
cac aac atg ggg gat cat gta act cgc ctt gat cat tgg gaa ccg gag	432
His Asn Met Gly Asp His Val Thr Arg Leu Asp His Trp Glu Pro Glu	
130 135 140	
ctg aat gaa gcc ata cca aac gac gag cgt gac acc acg atg cct gta	480
Leu Asn Glu Ala Ile Pro Asn Asp Glu Arg Asp Thr Thr Met Pro Val	
145 150 155 160	
gca atg gca aca acg ttg cgc aaa cta tta act ggc gaa cta ctt act	528
Ala Met Ala Thr Thr Leu Arg Lys Leu Leu Thr Gly Glu Leu Leu Thr	
165 170 175	
cta gct tcc cgg caa caa tta ata gac tgg atg gag gcg gat aaa gtt	576
Leu Ala Ser Arg Gln Gln Leu Ile Asp Trp Met Glu Ala Asp Lys Val	
180 185 190	
gca gga cca ctt ctg cgc tcg gcc ctt ccg gct ggc tgg ttt att gct	624
Ala Gly Pro Leu Leu Arg Ser Ala Leu Pro Ala Gly Trp Phe Ile Ala	
195 200 205	
gat aaa tct gga gcc ggt gag cgt ggg tct cgc ggt atc att gca gca	672
Asp Lys Ser Gly Ala Gly Glu Arg Gly Ser Arg Gly Ile Ile Ala Ala	
210 215 220	

ctg ggg cca gat ggt aag ccc tcc cgt atc gta gtt atc tac acg acg 720
 Leu Gly Pro Asp Gly Lys Pro Ser Arg Ile Val Val Ile Tyr Thr Thr
 225 230 235 240

ggg agt cag gca act atg gat gaa cga aat aga cag atc gct gag ata 768
 Gly Ser Gln Ala Thr Met Asp Glu Arg Asn Arg Gln Ile Ala Glu Ile
 245 250 255

ggt gcc tca ctg att aag cat tgg 792
 Gly Ala Ser Leu Ile Lys His Trp
 260

<210> 7

<211> 786

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)...(786)

<223> cloning vector

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ggg atc ttt gca ttg gat aca ggt aca aac cgg acg gta gcg tat cgg 96
 Gly Ile Phe Ala Leu Asp Thr Gly Thr Asn Arg Thr Val Ala Tyr Arg
 20 25 30

ccg gat gag cgt ttt gct ttt gct tcg acg att aag gct tta act gta 144
 Pro Asp Glu Arg Phe Ala Phe Ala Ser Thr Ile Lys Ala Leu Thr Val
 35 40 45

ggc gtg ctt ttg caa cag aaa tca ata gaa gat ctg aac cag aga ata 192
 Gly Val Leu Leu Gln Gln Lys Ser Ile Glu Asp Leu Asn Gln Arg Ile
 50 55 60

aca tat aca cgt gat gat ctt gta aac tac aac ccg att acg gaa aag 240
 Thr Tyr Thr Arg Asp Asp Leu Val Asn Tyr Asn Pro Ile Thr Glu Lys
 65 70 75 80

cac gtt gat acg gga atg acg ctc aaa gag ctt gcg gat gct tcg ctt 288
 His Val Asp Thr Gly Met Thr Leu Lys Glu Leu Ala Asp Ala Ser Leu
 85 90 95

cga tat agt gac aat gcg gca cag aat ctc att ctt aaa caa att ggc 336
 Arg Tyr Ser Asp Asn Ala Ala Gln Asn Leu Ile Leu Lys Gln Ile Gly
 100 105 110

gga cct gaa agt ttg aaa aag gaa ctg agg aag att ggt gat gag gtt 384
 Gly Pro Glu Ser Leu Lys Lys Glu Leu Arg Lys Ile Gly Asp Glu Val
 115 120 125

aca aat ccc gaa cga ttc gaa cca gag tta aat gaa gtg aat ccg ggt 432
 Thr Asn Pro Glu Arg Phe Glu Pro Glu Leu Asn Glu Val Asn Pro Gly
 130 135 140

gaa act cag gat acc agt aca gca aga gca ctt gtc aca agc ctt cga 480
Glu Thr Gln Asp Thr Ser Thr Ala Arg Ala Leu Val Thr Ser Leu Arg
145 150 155 160

gcc ttt gct ctt gaa gat aaa ctt cca agt gaa aaa cgc gag ctt tta 528
Ala Phe Ala Leu Glu Asp Lys Leu Pro Ser Glu Lys Arg Glu Leu Leu
165 170 175

atc gat tgg atg aaa cga aat acc act gga gac gcc tta atc cgt gcc 576
Ile Asp Trp Met Lys Arg Asn Thr Thr Gly Asp Ala Leu Ile Arg Ala
180 185 190

gga gcg gca tca tat gga acc cgg aat gac att gcc atc att tgg ccg 624
Gly Ala Ala Ser Tyr Gly Thr Arg Asn Asp Ile Ala Ile Ile Trp Pro
195 200 205

cca aaa gga gat cct gtc ggt gtg ccg gac ggt tgg gaa gtg gct gat 672
Pro Lys Gly Asp Pro Val Gly Val Pro Asp Gly Trp Glu Val Ala Asp
210 215 220

aaa act gtt ctt gca gta tta tcc agc agg gat aaa aag gac gcc aag 720
Lys Thr Val Leu Ala Val Leu Ser Ser Arg Asp Lys Lys Asp Ala Lys
225 230 235 240

tat	gat	gat	aaa	ctt	att	gca	gag	gca	aca	aag	gtg	gta	atg	aaa	gcc	768
Tyr	Asp	Asp	Lys	Leu	Ile	Ala	Glu	Ala	Thr	Lys	Val	Val	Met	Lys	Ala	
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 Leu Asn Met Asn Gly Lys
 260

<210> 8

<211> 720

<212> DNA

<213> Aequorea victoria

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ggcaagctga	ccctgaagtt	catctgcacc	accggcaagc	tgcccgtgcc	ctggcccacc	180
ctcgtgacca	ccttctccta	cggcgtgcag	tgcttcagcc	gctaccccca	ccacatgaag	240
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aacctggagt	acaactacaa	cagccacaac	gtctatatca	tggccgacaa	gcagaagaac	480
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gaccactacc	agcagaacac	ccccatcggc	gacggccccg	tgtctgtgcc	cgacaaccac	600
tacctgagca	ccagtcgcgc	cctgagcaaa	gaccccaacg	agaagcgcca	tcacatggtc	660
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<210> 9

<211> 690

<212> DNA

<213> Anemonia majano

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gacatactat	ctacagtgtt	caaatatgga	aatcgatgct	ttactgcgta	tcctaccagt	240
atgccccgact	atttcaaaca	agcatttcct	gacggaatgt	catatgaaag	gacttttacc	300
tatgaagatg	gaggagtgtg	tacagccagt	tgggaaataa	gccttaaagg	caactgcttt	360
gagcacaat	ccacgtttca	tggagtgaac	tttctgtctg	atggacctgt	gatggcgaag	420
aagacaactg	gttgggaccc	atcttttgag	aaaatgactg	tctgcgatgg	aatattgaag	480
ggtgatgtca	ccgcgttcct	catgctgcaa	ggaggtggca	attacagatg	ccaattccac	540
acttcttaca	agacaaaaaa	accggtgacg	atgccacca	accatgtggt	ggaacatcgc	600
attgcgagga	ccgaccttga	caaaggtggc	aacagtgttc	agctgacgga	gcacgctgtt	660
gcacatataa	cctctgttgt	ccctttctga				690

<210> 10

<211> 696

<212> DNA

<213> Zoanthus sp.

<400> 10

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gactatttca	agaactcgtg	tcctgctgga	tatacatggg	acagggtcttt	tctctttgag	300
gatggagcag	tttgcataatg	taatgcagat	ataacagtga	gtgttgaaga	aaactgcatg	360
tatcatgagt	ccaaatttta	tggagtgaat	tttctgtctg	atggacctgt	gatgaaaaag	420
atgacagata	actgggagcc	atcctgcgag	aagatcatat	cagtacctaa	gcaggggata	480
ttgaaagggg	atgtctccat	gtacctcctt	ctgaaggatg	gtgggcgttt	acggtgccaa	540
ttcgacacag	tttacaaagc	aaagtctgtg	ccaagaaaga	tgccggactg	gcacttcata	600
cagcataagc	tcacccgtga	agaccgcagc	gatgctaaga	atcagaaatg	gcacttgaca	660
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<210> 11

<211> 696

<212> DNA

<213> Zoanthus sp.

<400> 11

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aaacagacta	ttaatctgtg	tgtgatcgaa	gggggaccat	tgccattttc	cgaagacata	180
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<211> 699

<212> DNA

<213> Discosoma striata

<400> 12

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<210> 13

<211> 678

<212> DNA

<213> *Discosoma* sp.

<400> 13

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<210> 14

<211> 801

<212> DNA

<213> *Clavularia* sp.

<400> 14

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28

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<400> 22

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<213> Artificial Sequence

<220>

<223> oligonucleotide cassette

<400> 45

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<400> 46

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<223> pcDNA3-1XUb-DEVD-Bla construct

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